



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SHYJAN, Andrew

(ii) TITLE OF INVENTION: NOVEL MULTIDRUG RESISTANCE-ASSOCIATED POLYPEPTIDE

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
(B) STREET: 28 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02109

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/061,400
(B) FILING DATE: 16-APRIL-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Elizabeth A. Hanley
(B) REGISTRATION NUMBER: 33,505
(C) REFERENCE/DOCKET NUMBER: MNI-056CP

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 116..4426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCTCATGCT CGGGAGCGTG GTTGAGCGGC TGGCGCGTT GTCCTGGAGC AGGGGCGCAG 60
GAATTCTGAT GTGAAACTAA CAGTCTGTGA GCCCTGGAAC CTCCACTCAG AGAAC ATG 118
Met
1
AAG GAT ATC GAC ATA GGA AAA GAG TAT ATC ATC CCC AGT CCT GGG TAT 166
Lys Asp Ile Asp Ile Gly Lys Glu Tyr Ile Ile Pro Ser Pro Gly Tyr
5 10 15
AGA AGT GTG AGG GAG AGA ACC AGC ACT TCT GGG ACG CAC AGA GAC CGT 214
Arg Ser Val Arg Glu Arg Thr Ser Thr Ser Gly Thr His Arg Asp Arg
20 25 30
GAA GAT TCC AAG TTC AGG AGA ACT CGA CCG TTG GAA TGC CAA GAT GCC 262
Glu Asp Ser Lys Phe Arg Arg Thr Arg Pro Leu Glu Cys Gln Asp Ala

35	40	45	
TTG GAA ACA GCA GCC CGA GCC GAG GGC CTC TCT CTT GAT GCC TCC ATG Leu Glu Thr Ala Ala Arg Ala Glu Gly Leu Ser Leu Asp Ala Ser Met 50 55 60 65			310
CAT TCT CAG CTC AGA ATC CTG GAT GAG GAG CAT CCC AAG GGA AAG TAC His Ser Gln Leu Arg Ile Leu Asp Glu Glu His Pro Lys Gly Lys Tyr 70 75 80			358
CAT CAT GGC TTG AGT GCT CTG AAG CCC ATC CGG ACT ACT TGC AAA CAC His His Gly Leu Ser Ala Leu Lys Pro Ile Arg Thr Thr Cys Lys His 85 90 95			406
CAG CAC CCA GTG GAC AAT GCT GGG CTT TTT TCC TGT ATG ACT TTT TCG Gln His Pro Val Asp Asn Ala Gly Leu Phe Ser Cys Met Thr Phe Ser 100 105 110			454
TGG CTT TCT CTG GCC CGT GTG GCC CAC AAG AAG GGG GAG CTC TCA Trp Leu Ser Ser Leu Ala Arg Val Ala His Lys Lys Gly Glu Leu Ser 115 120 125			502
ATG GAA GAC GTG TGG TCT CTG TCC AAG CAC GAG TCT TCT GAC GTG AAC Met Glu Asp Val Trp Ser Leu Ser Lys His Glu Ser Ser Asp Val Asn 130 135 140 145			550
TGC AGA AGA CTA GAG AGA CTG TGG CAA GAA GAG CTG AAT GAA GTT GGG Cys Arg Arg Leu Glu Arg Leu Trp Gln Glu Glu Leu Asn Glu Val Gly 150 155 160			598
CCA GAC GCT GCT TCC CTG CGA AGG GTT GTG TGG ATC TTC TGC CGC ACC Pro Asp Ala Ala Ser Leu Arg Arg Val Val Trp Ile Phe Cys Arg Thr 165 170 175			646
AGG CTC ATC CTG TCC ATC GTG TGC CTG ATG ATC ACG CAG CTG GCT GGC Arg Leu Ile Leu Ser Ile Val Cys Leu Met Ile Thr Gln Leu Ala Gly 180 185 190			694
TTC AGT GGA CCA GCC TTC ATG GTG AAA CAC CTC TTG GAG TAT ACC CAG Phe Ser Gly Pro Ala Phe Met Val Lys His Leu Leu Glu Tyr Thr Gln 195 200 205			742
GCA ACA GAG TCT AAC CTG CAG TAC AGC TTG TTG TTA GTG CTG GGC CTC Ala Thr Glu Ser Asn Leu Gln Tyr Ser Leu Leu Leu Val Leu Gly Leu 210 215 220 225			790
CTC CTG ACG GAA ATC GTG CGG TCT TGG TCG CTT GCA CTG ACT TGG GCA Leu Leu Thr Glu Ile Val Arg Ser Trp Ser Leu Ala Leu Thr Trp Ala 230 235 240			838
TTG AAT TAC CGA ACC GGT GTC CGC TTG CGG GGG GCC ATC CTA ACC ATG Leu Asn Tyr Arg Thr Gly Val Arg Leu Arg Gly Ala Ile Leu Thr Met 245 250 255			886
GCA TTT AAG AAG ATC CTT AAG TTA AAG AAC ATT AAA GAG AAA TCC CTG Ala Phe Lys Lys Ile Leu Lys Leu Lys Asn Ile Lys Glu Lys Ser Leu 260 265 270			934
GGT GAG CTC ATC AAC ATT TGC TCC AAC GAT GGG CAG AGA ATG TTT GAG Gly Glu Leu Ile Asn Ile Cys Ser Asn Asp Gly Gln Arg Met Phe Glu 275 280 285			982
GCA GCA GCC GTT GGC AGC CTG CTG GCT GGA GGA CCC GTT GTT GCC ATC Ala Ala Ala Val Gly Ser Leu Leu Ala Gly Gly Pro Val Val Ala Ile 290 295 300 305			1030
TTA GGC ATG ATT TAT AAT GTA ATT ATT CTG GGA CCA ACA GGC TTC CTG Leu Gly Met Ile Tyr Asn Val Ile Ile Leu Gly Pro Thr Gly Phe Leu 310 315 320			1078
GGA TCA GCT GTT TTT ATC CTC TTT TAC CCA GCA ATG ATG TTT GCA TCA Gly Ser Ala Val Phe Ile Leu Phe Tyr Pro Ala Met Met Phe Ala Ser			1126

B1
CMY

325	330	335	
CGG CTC ACA GCA TAT TTC AGG AGA AAA TGC GTG GCC GCC ACG GAT GAA Arg Leu Thr Ala Tyr Phe Arg Arg Lys Cys Val Ala Ala Thr Asp Glu 340 345 350			1174
CGT GTC CAG AAG ATG AAT GAA GTT CTT ACT TAC ATT AAA TTT ATC AAA Arg Val Gln Lys Met Asn Glu Val Leu Thr Tyr Ile Lys Phe Ile Lys 355 360 365			1222
ATG TAT GCC TGG GTC AAA GCA TTT TCT CAG AGT GTT CAG AAA ATC CGC Met Tyr Ala Trp Val Lys Ala Phe Ser Gln Ser Val Gln Lys Ile Arg 370 375 380 385			1270
GAG GAG GAG CGT CGG ATA TTG GAA AAA GCC GGG TAC TTC CAG AGC ATC Glu Glu Glu Arg Arg Ile Leu Glu Lys Ala Gly Tyr Phe Gln Ser Ile 390 395 400			1318
ACT GTG GGT GTG GCT CCC ATT GTG GTG GTG ATT GCC AGC GTG GTG ACC Thr Val Gly Val Ala Pro Ile Val Val Val Ile Ala Ser Val Val Thr 405 410 415			1366
TTC TCT GTT CAT ATG ACC CTG GGC TTC GAT CTG ACA GCA GCA CAG GCT Phe Ser Val His Met Thr Leu Gly Phe Asp Leu Thr Ala Ala Gln Ala 420 425 430			1414
TTC ACA GTG GTG ACA GTC TTC AAT TCC ATG ACT TTT GCT TTG AAA GTA Phe Thr Val Val Thr Val Phe Asn Ser Met Thr Phe Ala Leu Lys Val 435 440 445			1462
ACA CCG TTT TCA GTA AAG TCC CTC TCA GAA GCC TCA GTG GCT GTT GAC Thr Pro Phe Ser Val Lys Ser Leu Ser Glu Ala Ser Val Ala Val Asp 450 455 460 465			1510
AGA TTT AAG AGT TTG TTT CTA ATG GAA GAG GTT CAC ATG ATA AAG AAC Arg Phe Lys Ser Leu Phe Leu Met Glu Glu Val His Met Ile Lys Asn 470 475 480			1558
AAA CCA GCC AGT CCT CAC ATC AAG ATA GAG ATG AAA AAT GCC ACC TTG Lys Pro Ala Ser Pro His Ile Lys Ile Glu Met Lys Asn Ala Thr Leu 485 490 495			1606
GCA TGG GAC TCC TCC CAC TCC AGT ATC CAG AAC TCG CCC AAG CTG ACC Ala Trp Asp Ser Ser His Ser Ser Ile Gln Asn Ser Pro Lys Leu Thr 500 505 510			1654
CCC AAA ATG AAA AAA GAC AAG AGG GCT TCC AGG GGC AAG AAA GAG AAG Pro Lys Met Lys Lys Asp Lys Arg Ala Ser Arg Gly Lys Lys Glu Lys 515 520 525			1702
GTG AGG CAG CTG CAG CGC ACT GAG CAT CAG GCG GTG CTG GCA GAG CAG Val Arg Gln Leu Gln Arg Thr Glu His Gln Ala Val Leu Ala Glu Gln 530 535 540 545			1750
AAA GGC CAC CTC CTC CTG GAC AGT GAC GAG CGG CCC AGT CCC GAA GAG Lys Gly His Leu Leu Asp Ser Asp Glu Arg Pro Ser Pro Glu Glu 550 555 560			1798
GAA GAA GGC AAG CAC ATC CAC CTG GGC CAC CTG CGC TTA CAG AGG ACA Glu Glu Gly Lys His Ile His Leu Gly His Leu Arg Leu Gln Arg Thr 565 570 575			1846
CTG CAC AGC ATC GAT CTG GAG ATC CAA GAG GGT AAA CTG GTT GGA ATC Leu His Ser Ile Asp Leu Glu Ile Gln Glu Gly Lys Leu Val Gly Ile 580 585 590			1894
TGC GGC AGT GTG GGA AGT GGA AAA ACC TCT CTC ATT TCA GCC ATT TTA Cys Gly Ser Val Gly Ser Gly Lys Thr Ser Leu Ile Ser Ala Ile Leu 595 600 605			1942
GGC CAG ATG ACG CTT CTA GAG GGC AGC ATT GCA ATC AGT GGA ACC TTC Gly Gln Met Thr Leu Leu Glu Gly Ser Ile Ala Ile Ser Gly Thr Phe			1990

610	615	620	625	
GCT TAT GTG GCC CAG CAG GCC TGG ATC CTC AAT GCT ACT CTG AGA GAC Ala Tyr Val Ala Gln Gln Ala Trp Ile Leu Asn Ala Thr Leu Arg Asp 630	635		640	2038
AAC ATC CTG TTT GGG AAG GAA TAT GAT GAA GAA AGA TAC AAC TCT GTG Asn Ile Leu Phe Gly Lys Glu Tyr Asp Glu Glu Arg Tyr Asn Ser Val 645	650	655		2086
CTG AAC AGC TGC TGC CTG AGG CCT GAC CTG GCC ATT CTT CCC AGC AGC Leu Asn Ser Cys Cys Leu Arg Pro Asp Leu Ala Ile Leu Pro Ser Ser 660	665	670		2134
GAC CTG ACG GAG ATT GGA GAG CGA GGA GCC AAC CTG AGC GGT GGG CAG Asp Leu Thr Glu Ile Gly Glu Arg Gly Ala Asn Leu Ser Gly Gly Gln 675	680	685		2182
CGC CAG AGG ATC AGC CTT GCC CGG GCC TTG TAT AGT GAC AGG AGC ATC Arg Gln Arg Ile Ser Leu Ala Arg Ala Leu Tyr Ser Asp Arg Ser Ile 690	695	700	705	2230
TAC ATC CTG GAC GAC CCC CTC AGT GCC TTA GAT GCC CAT GTG GGC AAC Tyr Ile Leu Asp Asp Pro Leu Ser Ala Leu Asp Ala His Val Gly Asn 710	715	720		2278
CAC ATC TTC AAT AGT GCT ATC CGG AAA CAT CTC AAG TCC AAG ACA GTT His Ile Phe Asn Ser Ala Ile Arg Lys His Leu Lys Ser Lys Thr Val 725	730	735		2326
CTG TTT GTT ACC CAC CAG TTA CAG TAC CTG GTT GAC TGT GAT GAA GTG Leu Phe Val Thr His Gln Leu Gln Tyr Leu Val Asp Cys Asp Glu Val 740	745	750		2374
ATC TTC ATG AAA GAG GGC TGT ATT ACG GAA AGA GGC ACC CAT GAG GAA Ile Phe Met Lys Glu Gly Cys Ile Thr Glu Arg Gly Thr His Glu Glu 755	760	765		2422
CTG ATG AAT TTA AAT GGT GAC TAT GCT ACC ATT TTT AAT AAC CTG TTG Leu Met Asn Leu Asn Gly Asp Tyr Ala Thr Ile Phe Asn Asn Leu Leu 770	775	780	785	2470
CTG GGA GAG ACA CCG CCA GTT GAG ATC AAT TCA AAA AAG GAA ACC AGT Leu Gly Glu Thr Pro Pro Val Glu Ile Asn Ser Lys Lys Glu Thr Ser 790	795	800		2518
GGT TCA CAG AAG AAG TCA CAA GAC AAG GGT CCT AAA ACA GGA TCA ATA Gly Ser Gln Lys Lys Ser Gln Asp Lys Gly Pro Lys Thr Gly Ser Ile 805	810	815		2566
AAG AAG GAA AAA GCA GTA AAG CCA GAG GAA GGG CAG CTT GTG CAG CTG Lys Lys Glu Lys Ala Val Lys Pro Glu Glu Gly Gln Leu Val Gln Leu 820	825	830		2614
GAA GAG AAA GGG CAG GGT TCA GTG CCC TGG TCA GTA TAT GGT GTC TAC Glú Glu Lys Gly Gln Gly Ser Val Pro Trp Ser Val Tyr Gly Val Tyr 835	840	845		2662
ATC CAG GCT GCT GGG GGC CCC TTG GCA TTC CTG GTT ATT ATG GCC CTT Ile Gln Ala Ala Gly Gly Pro Leu Ala Phe Leu Val Ile Met Ala Leu 850	855	860	865	2710
TTC ATG CTG AAT GTA GGC AGC ACC GCC TTC AGC ACC TGG TGG TTG AGT Phe Met Leu Asn Val Gly Ser Thr Ala Phe Ser Thr Trp Trp Leu Ser 870	875	880		2758
TAC TGG ATC AAG CAA GGA AGC GGG AAC ACC ACT GTG ACT CGA GGG AAC Tyr Trp Ile Lys Gln Gly Ser Gly Asn Thr Thr Val Thr Arg Gly Asn 885	890	895		2806
GAG ACC TCG GTG AGT GAC AGC ATG AAG GAC AAT CCT CAT ATG CAG TAC Glu Thr Ser Val Ser Asp Ser Met Lys Asp Asn Pro His Met Gln Tyr				2854

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Gmt

900	905	910														
TAT	GCC	AGC	ATC	TAC	GCC	CTC	TCC	ATG	GCA	GTC	ATG	CTG	ATC	CTG	AAA	2902
Tyr	Ala	Ser	Ile	Tyr	Ala	Leu	Ser	Met	Ala	Val	Met	Leu	Ile	Leu	Lys	
915					920						925					
GCC	ATT	CGA	GGA	GTT	GTC	TTT	GTC	AAG	GGC	ACG	CTG	CGA	GCT	TCC	TCC	2950
Ala	Ile	Arg	Gly	Val	Val	Phe	Val	Lys	Gly	Thr	Leu	Arg	Ala	Ser	Ser	
930				935					940		945					
CGG	CTG	CAT	GAC	GAG	CTT	TTC	CGA	AGG	ATC	CTT	CGA	AGC	CCT	ATG	AAG	2998
Arg	Leu	His	Asp	Glu	Leu	Phe	Arg	Arg	Ile	Leu	Arg	Ser	Pro	Met	Lys	
					950			955			960					
TTT	TTT	GAC	ACG	ACC	CCC	ACA	GGG	AGG	ATT	CTC	AAC	AGG	TTT	TCC	AAA	3046
Phe	Phe	Asp	Thr	Thr	Pro	Thr	Gly	Arg	Ile	Leu	Asn	Arg	Phe	Ser	Lys	
					965			970			975					
GAC	ATG	GAT	GAA	GTT	GAC	GTG	CGG	CTG	CCG	TTC	CAG	GCC	GAG	ATG	TTC	3094
Asp	Met	Asp	Glu	Val	Asp	Val	Arg	Leu	Pro	Phe	Gln	Ala	Glu	Met	Phe	
				980			985			990						
ATC	CAG	AAC	GTT	ATC	CTG	GTG	TTC	TTC	TGT	GTG	GGA	ATG	ATC	GCA	GGA	3142
Ile	Gln	Asn	Val	Ile	Leu	Val	Phe	Phe	Cys	Val	Gly	Met	Ile	Ala	Gly	
				995			1000			1005						
GTC	TTC	CCG	TGG	TTC	CTT	GTG	GCA	GTG	GGG	CCC	CTT	GTC	ATC	CTC	TTT	3190
Val	Phe	Pro	Trp	Phe	Leu	Val	Ala	Val	Gly	Pro	Leu	Val	Ile	Leu	Phe	
	1010				1015				1020			1025				
TCA	GTC	CTG	CAC	ATT	GTC	TCC	AGG	GTC	CTG	ATT	CGG	GAG	CTG	AAG	CGT	3238
Ser	Val	Leu	His	Ile	Val	Ser	Arg	Val	Leu	Ile	Arg	Glu	Leu	Lys	Arg	
				1030				1035			1040					
CTG	GAC	AAT	ATC	ACG	CAG	TCA	CCT	TTC	CTC	TCC	CAC	ATC	ACG	TCC	AGC	3286
Leu	Asp	Asn	Ile	Thr	Gln	Ser	Pro	Phe	Leu	Ser	His	Ile	Thr	Ser	Ser	
				1045				1050			1055					
ATA	CAG	GGC	CTT	GCC	ACC	ATC	CAC	GCC	TAC	AAT	AAA	GGG	CAG	GAG	TTT	3334
Ile	Gln	Gly	Leu	Ala	Thr	Ile	His	Ala	Tyr	Asn	Lys	Gly	Gln	Glu	Phe	
			1060			1065				1070						
CTG	CAC	AGA	TAC	CAG	GAG	CTG	CTG	GAT	GAC	AAC	CAA	GCT	CCT	TTT	TTT	3382
Leu	His	Arg	Tyr	Gln	Glu	Leu	Leu	Asp	Asp	Asn	Gln	Ala	Pro	Phe	Phe	
			1075			1080				1085						
TTG	TTT	ACG	TGT	GCG	ATG	CGG	TGG	CTG	GCT	GTG	CGG	CTG	GAC	CTC	ATC	3430
Leu	Phe	Thr	Cys	Ala	Met	Arg	Trp	Leu	Ala	Val	Arg	Leu	Asp	Leu	Ile	
	1090				1095				1100			1105				
AGC	ATC	GCC	CTC	ATC	ACC	ACC	ACG	GGG	CTG	ATG	ATC	GTT	CTT	ATG	CAC	3478
Ser	Ile	Ala	Leu	Ile	Thr	Thr	Thr	Gly	Leu	Met	Ile	Val	Leu	Met	His	
				1110				1115			1120					
GGG	CAG	ATT	CCC	CCA	GCC	TAT	GCG	GGT	CTC	GCC	ATC	TCT	TAT	GCT	GTC	3526
Gly	Gln	Ile	Pro	Pro	Ala	Tyr	Ala	Gly	Leu	Ala	Ile	Ser	Tyr	Ala	Val	
			1125				1130				1135					
CAG	TTA	ACG	GGG	CTG	TTC	CAG	TTT	ACG	GTC	AGA	CTG	GCA	TCT	GAG	ACA	3574
Gln	Leu	Thr	Gly	Leu	Phe	Gln	Phe	Thr	Val	Arg	Leu	Ala	Ser	Glu	Thr	
	1140				1145				1150							
GAA	GCT	CGA	TTC	ACC	TCG	GTG	GAG	AGG	ATC	AAT	CAC	TAC	ATT	AAG	ACT	3622
Glu	Ala	Arg	Phe	Thr	Ser	Val	Glu	Arg	Ile	Asn	His	Tyr	Ile	Lys	Thr	
	1155				1160				1165							
CTG	TCC	TTG	GAA	GCA	CCT	GCC	AGA	ATT	AAG	AAC	AAG	GCT	CCC	TCC	CCT	3670
Leu	Ser	Leu	Glu	Ala	Pro	Ala	Arg	Ile	Lys	Asn	Lys	Ala	Pro	Ser	Pro	
	1170				1175				1180			1185				
GAC	TGG	CCC	CAG	GAG	GGA	GAG	GTG	ACC	TTT	GAG	AAC	GCA	GAG	ATG	AGG	3718
Asp	Trp	Pro	Gln	Glu	Gly	Glu	Val	Thr	Phe	Glu	Asn	Ala	Glu	Met	Arg	

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Cn/
J

1190	1195	1200	
TAC CGA GAA AAC CTC CCT CTC GTC CTA AAG AAA GTA TCC TTC ACG ATC Tyr Arg Glu Asn Leu Pro Leu Val Leu Lys Lys Val Ser Phe Thr Ile 1205	1210	1215	3766
AAA CCT AAA GAG AAG ATT GGC ATT GTG GGG CGG ACA GGA TCA GGG AAG Lys Pro Lys Glu Lys Ile Gly Ile Val Gly Arg Thr Gly Ser Gly Lys 1220	1225	1230	3814
TCC TCG CTG GGG ATG GCC CTC TTC CGT CTG GTG GAG TTA TCT GGA GGC Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val Glu Leu Ser Gly Gly 1235	1240	1245	3862
TGC ATC AAG ATT GAT GGA GTG AGA ATC AGT GAT ATT GGC CTT GCC GAC Cys Ile Lys Ile Asp Gly Val Arg Ile Ser Asp Ile Gly Leu Ala Asp 1250	1255	1260	3910
CTC CGA AGC AAA CTC TCT ATC ATT CCT CAA GAG CCG GTG CTG TTC AGT Leu Arg Ser Lys Leu Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Ser 1270	1275	1280	3958
GGC ACT GTC AGA TCA AAT TTG GAC CCC TTC AAC CAG TAC ACT GAA GAC Gly Thr Val Arg Ser Asn Leu Asp Pro Phe Asn Gln Tyr Thr Glu Asp 1285	1290	1295	4006
CAG ATT TGG GAT GCC CTG GAG AGG ACA CAC ATG AAA GAA TGT ATT GCT Gln Ile Trp Asp Ala Leu Glu Arg Thr His Met Lys Glu Cys Ile Ala 1300	1305	1310	4054
CAG CTA CCT CTG AAA CTT GAA TCT GAA GTG ATG GAG AAT GGG GAT AAC Gln Leu Pro Leu Lys Leu Glu Ser Glu Val Met Glu Asn Gly Asp Asn 1315	1320	1325	4102
TTC TCA GTG GGG GAA CGG CAG CTC TTG TGC ATA GCT AGA GCC CTG CTC Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Ile Ala Arg Ala Leu Leu 1330	1335	1340	4150
CGC CAC TGT AAG ATT CTG ATT TTA GAT GAA GCC ACA GCT GCC ATG GAC Arg His Cys Lys Ile Leu Ile Leu Asp Glu Ala Thr Ala Ala Met Asp 1350	1355	1360	4198
ACA GAG ACA GAC TTA TTG ATT CAA GAG ACC ATC CGA GAA GCA TTT GCA Thr Glu Thr Asp Leu Leu Ile Gln Glu Thr Ile Arg Glu Ala Phe Ala 1365	1370	1375	4246
GAC TGT ACC ATG CTG ACC ATT GCC CAT CGC CTG CAC ACG GTT CTA GGC Asp Cys Thr Met Leu Thr Ile Ala His Arg Leu His Thr Val Leu Gly 1380	1385	1390	4294
TCC GAT AGG ATT ATG GTG CTG GCC CAG GGA CAG GTG GTG GAG TTT GAC Ser Asp Arg Ile Met Val Leu Ala Gln Gly Gln Val Val Glu Phe Asp 1395	1400	1405	4342
ACC CCA TCG GTC CTT CTG TCC AAC GAC AGT TCC CGA TTC TAT GCC ATG Thr Pro Ser Val Leu Leu Ser Asn Asp Ser Ser Arg Phe Tyr Ala Met 1410	1415	1420	4390
TTT GCT GCT GCA GAG AAC AAG GTC GCT GTC AAG GGC TGACTCCTCC Phe Ala Ala Ala Glu Asn Lys Val Ala Val Lys Gly 1430	1435		4436
CTGTTGACGA AGTCTCTTTT CTTTAGAGCA TTGCCATTCC CTGCCTGGGG CGGGCCCTT			4496
CATCGCGTCC TCCTACCGAA ACCTTGCCTT TCTCGATTTT ATCTTCGCA CAGCAGTTCC			4556
GGATTGGCTT GTGTGTTCA CTTTAGGGA GAGTCATATT TTGATTATTG TATTATTCC			4616
ATATTCATGT AAACAAAATT TAGTTTTGT TCTTAATTGC ACTCTAAAAG GTTCAGGGAA			4676
CCGTTATTAT AATTGTATCA GAGGCCTATA ATGAAGCTTT ATACGTGTAG CTATATCTAT			4736

B
Gmt

ATATAATTCT GTACATAGCC TATATTTACA GTGAAAATGT AAGCTGTTA TTTTATATTA 4796
AAATAAGCAC TGTGCTAAAAA AAAAAAAA AAAAAAAA AGGGCGGCCG C 4847

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1437 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Asp Ile Asp Ile Gly Lys Glu Tyr Ile Ile Pro Ser Pro Gly
1 5 10 15
Tyr Arg Ser Val Arg Glu Arg Thr Ser Thr Ser Gly Thr His Arg Asp
20 25 30
Arg Glu Asp Ser Lys Phe Arg Arg Thr Arg Pro Leu Glu Cys Gln Asp
35 40 45
Ala Leu Glu Thr Ala Ala Arg Ala Glu Gly Leu Ser Leu Asp Ala Ser
50 55 60
Met His Ser Gln Leu Arg Ile Leu Asp Glu Glu His Pro Lys Gly Lys
65 70 75 80
Tyr His His Gly Leu Ser Ala Leu Lys Pro Ile Arg Thr Thr Cys Lys
85 90 95
His Gln His Pro Val Asp Asn Ala Gly Leu Phe Ser Cys Met Thr Phe
100 105 110
Ser Trp Leu Ser Ser Leu Ala Arg Val Ala His Lys Lys Gly Glu Leu
115 120 125
Ser Met Glu Asp Val Trp Ser Leu Ser Lys His Glu Ser Ser Asp Val
130 135 140
Asn Cys Arg Arg Leu Glu Arg Leu Trp Gln Glu Glu Leu Asn Glu Val
145 150 155 160
Gly Pro Asp Ala Ala Ser Leu Arg Arg Val Val Trp Ile Phe Cys Arg
165 170 175
Thr Arg Leu Ile Leu Ser Ile Val Cys Leu Met Ile Thr Gln Leu Ala
180 185 190
Gly Phe Ser Gly Pro Ala Phe Met Val Lys His Leu Leu Glu Tyr Thr
195 200 205
Gln Ala Thr Glu Ser Asn Leu Gln Tyr Ser Leu Leu Val Leu Gly
210 215 220
Leu Leu Leu Thr Glu Ile Val Arg Ser Trp Ser Leu Ala Leu Thr Trp
225 230 235 240
Ala Leu Asn Tyr Arg Thr Gly Val Arg Leu Arg Gly Ala Ile Leu Thr
245 250 255
Met Ala Phe Lys Lys Ile Leu Lys Leu Lys Asn Ile Lys Glu Lys Ser
260 265 270
Leu Gly Glu Leu Ile Asn Ile Cys Ser Asn Asp Gly Gln Arg Met Phe
275 280 285
Glu Ala Ala Ala Val Gly Ser Leu Leu Ala Gly Gly Pro Val Val Ala
290 295 300

Ile Leu Gly Met Ile Tyr Asn Val Ile Leu Gly Pro Thr Gly Phe
305 310 315 320

Leu Gly Ser Ala Val Phe Ile Leu Phe Tyr Pro Ala Met Met Phe Ala
325 330 335

Ser Arg Leu Thr Ala Tyr Phe Arg Arg Lys Cys Val Ala Ala Thr Asp
340 345 350

Glu Arg Val Gln Lys Met Asn Glu Val Leu Thr Tyr Ile Lys Phe Ile
355 360 365

Lys Met Tyr Ala Trp Val Lys Ala Phe Ser Gln Ser Val Gln Lys Ile
370 375 380

Arg Glu Glu Glu Arg Arg Ile Leu Glu Lys Ala Gly Tyr Phe Gln Ser
385 390 395 400

Ile Thr Val Gly Val Ala Pro Ile Val Val Val Ile Ala Ser Val Val
405 410 415

Thr Phe Ser Val His Met Thr Leu Gly Phe Asp Leu Thr Ala Ala Gln
420 425 430

Ala Phe Thr Val Val Thr Val Phe Asn Ser Met Thr Phe Ala Leu Lys
435 440 445

Val Thr Pro Phe Ser Val Lys Ser Leu Ser Glu Ala Ser Val Ala Val
450 455 460

Asp Arg Phe Lys Ser Leu Phe Leu Met Glu Glu Val His Met Ile Lys
465 470 475 480

Asn Lys Pro Ala Ser Pro His Ile Lys Ile Glu Met Lys Asn Ala Thr
485 490 495

Leu Ala Trp Asp Ser Ser His Ser Ser Ile Gln Asn Ser Pro Lys Leu
500 505 510

Thr Pro Lys Met Lys Lys Asp Lys Arg Ala Ser Arg Gly Lys Lys Glu
515 520 525

Lys Val Arg Gln Leu Gln Arg Thr Glu His Gln Ala Val Leu Ala Glu
530 535 540

Gln Lys Gly His Leu Leu Asp Ser Asp Glu Arg Pro Ser Pro Glu
545 550 555 560

Glu Glu Glu Gly Lys His Ile His Leu Gly His Leu Arg Leu Gln Arg
565 570 575

Thr Leu His Ser Ile Asp Leu Glu Ile Gln Glu Gly Lys Leu Val Gly
580 585 590

Ile Cys Gly Ser Val Gly Ser Gly Lys Thr Ser Leu Ile Ser Ala Ile
595 600 605

Leu Gly Gln Met Thr Leu Leu Glu Gly Ser Ile Ala Ile Ser Gly Thr
610 615 620

Phe Ala Tyr Val Ala Gln Gln Ala Trp Ile Leu Asn Ala Thr Leu Arg
625 630 635 640

Asp Asn Ile Leu Phe Gly Lys Glu Tyr Asp Glu Glu Arg Tyr Asn Ser
645 650 655

Val Leu Asn Ser Cys Cys Leu Arg Pro Asp Leu Ala Ile Leu Pro Ser
660 665 670

Ser Asp Leu Thr Glu Ile Gly Glu Arg Gly Ala Asn Leu Ser Gly Gly
675 680 685

Gln Arg Gln Arg Ile Ser Leu Ala Arg Ala Leu Tyr Ser Asp Arg Ser
690 695 700

Ile Tyr Ile Leu Asp Asp Pro Leu Ser Ala Leu Asp Ala His Val Gly
705 710 715 720

Asn His Ile Phe Asn Ser Ala Ile Arg Lys His Leu Lys Ser Lys Thr
725 730 735

Val Leu Phe Val Thr His Gln Leu Gln Tyr Leu Val Asp Cys Asp Glu
740 745 750

Val Ile Phe Met Lys Glu Gly Cys Ile Thr Glu Arg Gly Thr His Glu
755 760 765

Glu Leu Met Asn Leu Asn Gly Asp Tyr Ala Thr Ile Phe Asn Asn Leu
770 775 780

Leu Leu Gly Glu Thr Pro Pro Val Glu Ile Asn Ser Lys Lys Glu Thr
785 790 795 800

Ser Gly Ser Gln Lys Lys Ser Gln Asp Lys Gly Pro Lys Thr Gly Ser
805 810 815

Ile Lys Lys Glu Lys Ala Val Lys Pro Glu Glu Gly Gln Leu Val Gln
820 825 830

Leu Glu Glu Lys Gly Gln Gly Ser Val Pro Trp Ser Val Tyr Gly Val
835 840 845

Tyr Ile Gln Ala Ala Gly Gly Pro Leu Ala Phe Leu Val Ile Met Ala
850 855 860

Leu Phe Met Leu Asn Val Gly Ser Thr Ala Phe Ser Thr Trp Trp Leu
865 870 875 880

Ser Tyr Trp Ile Lys Gln Gly Ser Gly Asn Thr Thr Val Thr Arg Gly
885 890 895

Asn Glu Thr Ser Val Ser Asp Ser Met Lys Asp Asn Pro His Met Gln
900 905 910

Tyr Tyr Ala Ser Ile Tyr Ala Leu Ser Met Ala Val Met Leu Ile Leu
915 920 925

Lys Ala Ile Arg Gly Val Val Phe Val Lys Gly Thr Leu Arg Ala Ser
930 935 940

Ser Arg Leu His Asp Glu Leu Phe Arg Arg Ile Leu Arg Ser Pro Met
945 950 955 960

Lys Phe Phe Asp Thr Thr Pro Thr Gly Arg Ile Leu Asn Arg Phe Ser
965 970 975

Lys Asp Met Asp Glu Val Asp Val Arg Leu Pro Phe Gln Ala Glu Met
980 985 990

Phe Ile Gln Asn Val Ile Leu Val Phe Phe Cys Val Gly Met Ile Ala
995 1000 1005

Gly Val Phe Pro Trp Phe Leu Val Ala Val Gly Pro Leu Val Ile Leu
1010 1015 1020

Phe Ser Val Leu His Ile Val Ser Arg Val Leu Ile Arg Glu Leu Lys
1025 1030 1035 1040

Arg Leu Asp Asn Ile Thr Gln Ser Pro Phe Leu Ser His Ile Thr Ser
1045 1050 1055

Ser Ile Gln Gly Leu Ala Thr Ile His Ala Tyr Asn Lys Gly Gln Glu
1060 1065 1070

Phe Leu His Arg Tyr Gln Glu Leu Leu Asp Asp Asn Gln Ala Pro Phe
1075 1080 1085

Phe Leu Phe Thr Cys Ala Met Arg Trp Leu Ala Val Arg Leu Asp Leu
1090 1095 1100

Ile Ser Ile Ala Leu Ile Thr Thr Thr Gly Leu Met Ile Val Leu Met
1105 1110 1115 1120

His Gly Gln Ile Pro Pro Ala Tyr Ala Gly Leu Ala Ile Ser Tyr Ala
1125 1130 1135

Val Gln Leu Thr Gly Leu Phe Gln Phe Thr Val Arg Leu Ala Ser Glu
1140 1145 1150

Thr Glu Ala Arg Phe Thr Ser Val Glu Arg Ile Asn His Tyr Ile Lys
1155 1160 1165

Thr Leu Ser Leu Glu Ala Pro Ala Arg Ile Lys Asn Lys Ala Pro Ser
1170 1175 1180

Pro Asp Trp Pro Gln Glu Gly Glu Val Thr Phe Glu Asn Ala Glu Met
1185 1190 1195 1200

Arg Tyr Arg Glu Asn Leu Pro Leu Val Leu Lys Lys Val Ser Phe Thr
1205 1210 1215

Ile Lys Pro Lys Glu Lys Ile Gly Ile Val Gly Arg Thr Gly Ser Gly
1220 1225 1230

Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val Glu Leu Ser Gly
1235 1240 1245

Gly Cys Ile Lys Ile Asp Gly Val Arg Ile Ser Asp Ile Gly Leu Ala
1250 1255 1260

Asp Leu Arg Ser Lys Leu Ser Ile Ile Pro Gln Glu Pro Val Leu Phe
1265 1270 1275 1280

Ser Gly Thr Val Arg Ser Asn Leu Asp Pro Phe Asn Gln Tyr Thr Glu
1285 1290 1295

Asp Gln Ile Trp Asp Ala Leu Glu Arg Thr His Met Lys Glu Cys Ile
1300 1305 1310

Ala Gln Leu Pro Leu Lys Leu Glu Ser Glu Val Met Glu Asn Gly Asp
1315 1320 1325

Asn Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Ile Ala Arg Ala Leu
1330 1335 1340

Leu Arg His Cys Lys Ile Leu Ile Leu Asp Glu Ala Thr Ala Ala Met
1345 1350 1355 1360

Asp Thr Glu Thr Asp Leu Leu Ile Gln Glu Thr Ile Arg Glu Ala Phe
1365 1370 1375

Ala Asp Cys Thr Met Leu Thr Ile Ala His Arg Leu His Thr Val Leu
1380 1385 1390

Gly Ser Asp Arg Ile Met Val Leu Ala Gln Gly Gln Val Val Glu Phe
1395 1400 1405

Asp Thr Pro Ser Val Leu Leu Ser Asn Asp Ser Ser Arg Phe Tyr Ala
1410 1415 1420

Met Phe Ala Ala Ala Glu Asn Lys Val Ala Val Lys Gly
1425 1430 1435

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GC GTCCGCCT AGAACGCAGA GATGAGGTAC CGAGAAAACC TCCCTCTCGT CCTAAAGAAA	60
GTATCCTTCA CGATCAAACC TAAAGAGAAG ATTGGCATTG TGGGGCGGAC AGGATCAGGG	120
AAGTCCTCGC TGGGGATGGC CCTCTTCCGT CTGGTGGAGT TATCTGGAGG CTGCATCAAG	180
ATTGATGGAG TGAGAACATCAG TGATATTGGC CTTGCCGACC TCCGAAGCAA ACTCTCTATC	240
ATTCCCTCAAG AGCCGGTGCT GTTCAGTGGC ACTGTCAGAT CAAATTTGGA CCCTTCAACC	300
AGTACACTGA AGACCAGATT TGGGATGCC TGGAAAGGAC ACACATGAAA GAATGTATTG	360
CTCCAGCTAC CTCCTGAAAC TTGAATCCTG AATTTGATGG AGAAATGGGG AAATAACTTC	420
TCCAGTTGGG GGAAACGGCA CTCTTGTTG CCATACCTAN ACC	463

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGCTGGTTCT CTCCCTCACA CTTC	24
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any
(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCGGCTCGG GCTGCTGTTT CCAA	24
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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGTGCTGGT GTTTGGAAGT AGTC	24
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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCAGAGAAG AAAGCCACGA AAAA

24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi)*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGCACACGA TGGACAGGAT GAGC

24